| ystemic nam | *Gene name* | Description | Fold change VPA+/VPA- | |
|---|---|---|---|---|
| | | | Inositol+ | Inositol- |
| YCR034W | *FEN1* | Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; mutations have regulatory effects on 1,3- | 2.46 | 2.86 |
| YLR372W | *SUR4* | Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers; involved in | 2.77 | 2.47 |
| YNR056C | *BIO5* | Putative transmembrane protein involved in the biotin biosynthesis pathway; responsible for uptake of 7-keto 8-aminopelargonic acid; BIO5 is in a cluster | – | -8.92 |
| YCL025C | *AGP1* | Low-affinity amino acid permease with broad substrate range, involved in uptake of asparagine, glutamine, and other amino acids; expression is | – | -3.77 |
| YKR039W | *GAP1* | General amino acid permease; localization to the plasma membrane is regulated by nitrogen source | – | -2.85 |
| YBR068C | *BAP2* | High-affinity leucine permease, functions as a branched-chain amino acid permease involved in the | – | -6.22 |
| YPL265W | *DIP5* | Dicarboxylic amino acid permease, mediates high-affinity and high-capacity transport of L-glutamate | -2.22 | -2.36 |
| YDL210W | *UGA4* | Permease that serves as a gamma-aminobutyrate (GABA) transport protein involved in the utilization of GABA as a nitrogen source; catalyzes the transport of | – | -2.26 |
| YEL063C | *CAN1* | Plasma membrane arginine permease, requires phosphatidyl ethanolamine (PE) for localization, | – | -2.31 |
| YPL274W | *SAM3* | High-affinity S-adenosylmethionine permease, required for utilization of S-adenosylmethionine as a | – | -13.79 |
| YDR518W | *EUG1* | Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of | – | 2.39 |
| YJL073W | *JEM1* | DnaJ-like chaperone required for nuclear membrane fusion during mating, localizes to the ER membrane; | – | 5.81 |
| YKL073W | *LHS1* | Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; nucleotide exchange factor for the ER | – | 3.50 |
| YCL043C | *PDI1* | Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in | – | 2.83 |
| YPL187W | *MF(ALPHA)1* | Mating pheromone alpha-factor, made by alpha cells; interacts with mating type a cells to induce cell cycle arrest and other responses leading to mating; also | 11.29 | – |
| YOR153W | *PDR5* | Plasma membrane ATP-binding cassette (ABC) transporter, multidrug transporter actively regulated by Pdr1p; also involved in steroid transport, cation | 10.09 | 12.10 |

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|---|---|---|---|---|
| YLR307W | *CDA1* | Chitin deacetylase, together with Cda2p involved in the biosynthesis ascospore wall component, | 8.54 | 8.31 |
| YJL116C | *NCA3* | Protein that functions with Nca2p to regulate mitochondrial expression of subunits 6 (Atp6p) and 8 (Atp8p ) of the Fo-F1 ATP synthase; member of the | 7.43 | – |
| YKL121W | *DGR2* | Protein of unknown function; null mutant is resistant to 2-deoxy-D-glucose and displays abnormally | 5.55 | 2.68 |
| YKL178C | *STE3* | Receptor for a factor pheromone, couples to MAP kinase cascade to mediate pheromone response; transcribed in alpha cells and required for mating by | 5.53 | – |
| YBR040W | *FIG1* | Integral membrane protein required for efficient mating; may participate in or regulate the low affinity Ca2+ influx system, which affects intracellular | 5.37 | – |
| YOL101C | *IZH4* | Membrane protein involved in zinc ion homeostasis, member of the four-protein IZH family, expression induced by fatty acids and altered zinc levels; | 5.35 | 5.88 |
| YEL057C | *YEL057C* | Protein of unknown function involved in telomere | 5.30 | – |
| YNL289W | *PCL1* | Cyclin, interacts with cyclin-dependent kinase Pho85p; member of the Pcl1,2-like subfamily, involved in the regulation of polarized growth and | 5.25 | – |
| YJR078W | *BNA2* | Putative tryptophan 2,3-dioxygenase or indoleamine 2,3-dioxygenase, required for de novo biosynthesis of NAD from tryptophan via kynurenine; interacts | 5.13 | – |
| YGR225W | *AMA1* | Activator of meiotic anaphase promoting complex (APC/C); Cdc20p family member; required for | 5.03 | 2.59 |
| YOR315W | *SFG1* | Nuclear protein, putative transcription factor required for growth of superficial pseudohyphae (which do not invade the agar substrate) but not for | 4.94 | – |
| YDR317W | *HIM1* | Protein of unknown function involved in DNA repair | 4.78 | – |
| YML027W | *YOX1* | Homeodomain-containing transcriptional repressor, binds to Mcm1p and to early cell cycle boxes (ECBs) in the promoters of cell cycle-regulated genes | 4.59 | – |
| YGL055W | *OLE1* | Delta(9) fatty acid desaturase, required for monounsaturated fatty acid synthesis and for normal | 4.59 | – |
| YER060W | *FCY21* | Putative purine-cytosine permease, very similar to | 4.56 | – |
| YPR119W | *CLB2* | B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the transition from G2 to M phase; accumulates during G2 and M, then | 4.54 | – |
| YOL014W | *YOL014W* | Putative protein of unknown function | 4.43 | 11.01 |
| YHL028W | *WSC4* | ER membrane protein involved in the translocation of soluble secretory proteins and insertion of membrane proteins into the ER membrane; may also | 4.22 | – |

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|---|---|---|---|---|
| YLR183C | *TOS4* | Forkhead Associated domain containing protein and putative transcription factor found associated with chromatin; target of SBF transcription factor; | 4.22 | 5.96 |
| YBR021W | *FUR4* | Uracil permease, localized to the plasma membrane; expression is tightly regulated by uracil levels and | 4.20 | – |
| YDL101C | *DUN1* | Cell-cycle checkpoint serine-threonine kinase required for DNA damage-induced transcription of certain target genes, phosphorylation of Rad55p and | 4.19 | – |
| YCL048W | *SPS22* | Protein of unknown function, redundant with Sps2p for the organization of the beta-glucan layer of the | 4.12 | 2.53 |
| YMR215W | *GAS3* | Putative 1,3-beta-glucanosyltransferase, has | 4.07 | |
| YKL216W | *URA1* | Dihydroorotate dehydrogenase, catalyzes the fourth enzymatic step in the de novo biosynthesis of | 3.93 | 4.66 |
| YKR090W | *PXL1* | LIM domain-containing protein that localizes to sites of polarized growth, required for selection and/or maintenance of polarized growth sites, may | 3.88 | |
| YPL081W | *RPS9A* | Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity | 3.88 | 3.15 |
| YJL158C | *CIS3* | Mannose-containing glycoprotein constituent of the cell wall; member of the PIR (proteins with internal | 3.85 | 3.06 |
| YMR199W | *CLN1* | G1 cyclin involved in regulation of the cell cycle; activates Cdc28p kinase to promote the G1 to S phase transition; late G1 specific expression depends | 3.80 | – |
| YPL256C | *CLN2* | G1 cyclin involved in regulation of the cell cycle; activates Cdc28p kinase to promote the G1 to S phase transition; late G1 specific expression depends | 3.80 | – |
| YHL024W | *RIM4* | Putative RNA-binding protein required for the expression of early and middle sporulation genes | 3.75 | – |
| YMR076C | *PDS5* | Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes, may | 3.75 | – |
| YHR184W | *SSP1* | Protein involved in the control of meiotic nuclear division and coordination of meiosis with spore | 3.66 | – |
| YLR012C | *YLR012C* | Putative protein of unknown function; YLR012C is not | 3.64 | – |
| YHR172W | *SPC97* | Component of the microtubule-nucleating Tub4p (gamma-tubulin) complex; interacts with Spc110p at | 3.56 | – |
| YJL037W | *IRC18* | Putative protein of unknown function; expression induced in respiratory-deficient cells and in carbon-limited chemostat cultures; similar to adjacent ORF, | 3.55 | – |
| YLR103C | *CDC45* | DNA replication initiation factor; recruited to MCM pre-RC complexes at replication origins; promotes release of MCM from Mcm10p, recruits elongation | 3.50 | – |

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| YHR154W | *RTT107* | Protein implicated in Mms22-dependent DNA repair during S phase, DNA damage induces phosphorylation by Mec1p at one or more SQ/TQ | 3.49 | – |
| YHR153C | *SPO16* | Meiosis-specific protein involved in synaptonemal complex assembly; implicated in regulation of | 3.49 | 5.79 |
| YDR451C | *YHP1* | One of two homeobox transcriptional repressors (see also Yox1p), that bind to Mcm1p and to early cell cycle box (ECB) elements of cell cycle regulated | 3.37 | – |
| YJL194W | *CDC6* | Essential ATP-binding protein required for DNA replication, component of the pre-replicative complex (pre-RC) which requires ORC to associate | 3.36 | – |
| YBR088C | *POL30* | Proliferating cell nuclear antigen (PCNA), functions as the sliding clamp for DNA polymerase delta; may function as a docking site for other proteins required | 3.36 | 5.26 |
| YJR053W | *BFA1* | Component of the GTPase-activating Bfa1p-Bub2p complex involved in multiple cell cycle checkpoint | 3.34 | 2.67 |
| YJR092W | *BUD4* | Protein involved in bud-site selection and required for axial budding pattern; localizes with septins to bud neck in mitosis and may constitute an axial | 3.33 | – |
| YDR146C | *SWI5* | Transcription factor that activates transcription of genes expressed at the M/G1 phase boundary and in G1 phase; localization to the nucleus occurs during | 3.33 | – |
| YDR042C | *YDR042C* | Putative protein of unknown function; expression is | 3.33 | – |
| YPL231W | *FAS2* | Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains the acyl-carrier protein domain and | 3.31 | 2.66 |
| YMR101C | *SRT1* | Cis-prenyltransferase involved in synthesis of long-chain dolichols (19-22 isoprene units; as opposed to Rer2p which synthesizes shorter-chain dolichols); | 3.30 | – |
| YNR030W | *ALG12* | Alpha-1,6-mannosyltransferase localized to the ER; responsible for the addition of the alpha-1,6 | 3.30 | – |
| YMR305C | *SCW10* | Cell wall protein with similarity to glucanases; may play a role in conjugation during mating based on | 3.30 | – |
| YOL151W | *GRE2* | 3-methylbutanal reductase and NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase); stress induced (osmotic, ionic, | 3.26 | – |
| YNL301C | *RPL18B* | Protein component of the large (60S) ribosomal subunit, identical to Rpl18Ap and has similarity to rat | 3.19 | 2.86 |
| YNR073C | *YNR073C* | Putative mannitol dehydrogenase | 3.17 | – |
| YMR144W | *YMR144W* | Putative protein of unknown function; localized to the nucleus; YMR144W is not an essential gene | 3.11 | – |

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| YDL003W | *MCD1* | Essential subunit of the cohesin complex required for sister chromatid cohesion in mitosis and meiosis; apoptosis induces cleavage and translocation of a C- | 3.10 | 3.70 |
| YCL026C-B | *HBN1* | Putative protein of unknown function; similar to bacterial nitroreductases; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and | 3.05 | 2.68 |
| YMR032W | *HOF1* | Bud neck-localized, SH3 domain-containing protein required for cytokinesis; regulates actomyosin ring dynamics and septin localization; interacts with the | 3.03 | – |
| YER187W | *YER187W* | Putative protein of unknown function; induced in | 2.98 | – |
| YJL092W | *SRS2* | DNA helicase and DNA-dependent ATPase involved in DNA repair, needed for proper timing of commitment to meiotic recombination and transition from Meiosis | 2.93 | – |
| YBR078W | *ECM33* | GPI-anchored protein of unknown function, has a possible role in apical bud growth; GPI-anchoring on the plasma membrane crucial to function; | 2.91 | – |
| YLR054C | *OSW2* | Protein of unknown function proposed to be involved | 2.89 | 2.17 |
| YMR303C | *ADH2* | Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; | 2.89 | – |
| YDL114W | *YDL114W* | Putative protein of unknown function with similarity to acyl-carrier-protein reductases; YDL114W is not an | 2.82 | – |
| YGR286C | *BIO2* | Biotin synthase, catalyzes the conversion of dethiobiotin to biotin, which is the last step of the | 2.79 | – |
| YOL132W | *GAS4* | 1,3-beta-glucanosyltransferase, involved with Gas2p in spore wall assembly; has similarity to Gas1p; | 2.77 | – |
| YAL061W | *BDH2* | Putative medium-chain alcohol dehydrogenase with similarity to BDH1; transcription induced by | 2.76 | – |
| YDR528W | *HLR1* | Protein involved in regulation of cell wall composition and integrity and response to osmotic stress; overproduction suppresses a lysis sensitive PKC | 2.75 | – |
| YIL123W | *SIM1* | Protein of the SUN family (Sim1p, Uth1p, Nca3p, Sun4p) that may participate in DNA replication, promoter contains SCB regulation box at -300 bp | 2.74 | – |
| YJL080C | *SCP160* | Essential RNA-binding G protein effector of mating response pathway, mainly associated with nuclear envelope and ER, interacts in mRNA-dependent | 2.72 | – |
| YBL031W | *SHE1* | Mitotic spindle protein that interacts with components of the Dam1 (DASH) complex, its effector Sli15p, and microtubule-associated protein | 2.71 | 2.20 |
| YBR092C | *PHO3* | Constitutively expressed acid phosphatase similar to Pho5p; brought to the cell surface by transport vesicles; hydrolyzes thiamin phosphates in the | 2.71 | – |
| YJL102W | *MEF2* | Mitochondrial elongation factor involved in | 2.70 | 3.61 |

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|---|---|---|---|---|
| YAR007C | *RFA1* | Subunit of heterotrimeric Replication Protein A (RPA), which is a highly conserved single-stranded DNA | 2.68 | 2.97 |
| YLR131C | *ACE2* | Transcription factor that activates expression of early G1-specific genes, localizes to daughter cell nuclei after cytokinesis and delays G1 progression in | 2.66 | 2.33 |
| YER095W | *RAD51* | Strand exchange protein, forms a helical filament with DNA that searches for homology; involved in the recombinational repair of double-strand breaks in | 2.66 | – |
| YOR049C | *RSB1* | Suppressor of sphingoid long chain base (LCB) sensitivity of an LCB-lyase mutation; putative integral membrane transporter or flippase that may transport | 2.65 | – |
| YDR503C | *LPP1* | Lipid phosphate phosphatase, catalyzes Mg(2+)-independent dephosphorylation of phosphatidic acid (PA), lysophosphatidic acid, and diacylglycerol | 2.62 | – |
| YBR184W | *YBR184W* | Putative protein of unknown function; YBR184W is | 2.62 | – |
| YPL248C | *GAL4* | DNA-binding transcription factor required for the activation of the GAL genes in response to galactose; | 2.58 | – |
| YER043C | *SAH1* | S-adenosyl-L-homocysteine hydrolase, catabolizes S-adenosyl-L-homocysteine which is formed after donation of the activated methyl group of S-adenosyl- | 2.57 | 2.62 |
| YDR497C | *ITR1* | Myo-inositol transporter with strong similarity to the minor myo-inositol transporter Itr2p, member of the sugar transporter superfamily; expression is | 2.57 | – |
| YER032W | *FIR1* | Protein involved in 3' mRNA processing, interacts | 2.56 | 2.28 |
| YPL127C | *HHO1* | Histone H1, a linker histone required for nucleosome packaging at restricted sites; suppresses DNA repair involving homologous recombination; not required | 2.55 | – |
| YER085C | *YER085C* | Putative protein of unknown function | 2.54 | – |
| YCR088W | *ABP1* | Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 | 2.54 | – |
| YNR019W | *ARE2* | Acyl-CoA:sterol acyltransferase, isozyme of Are1p; endoplasmic reticulum enzyme that contributes the | 2.52 | 2.74 |
| YLR045C | *STU2* | Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates microtubule dynamics during spindle orientation and metaphase | 2.51 | – |
| YBR069C | *TAT1* | Amino acid transport protein for valine, leucine, isoleucine, and tyrosine, low-affinity tryptophan and | 2.51 | – |
| YEL070W | *DSF1* | Deletion suppressor of mpt5 mutation | 2.50 | – |
| YDR501W | *PLM2* | Forkhead Associated domain containing protein and putative transcription factor found associated with chromatin; target of SBF transcription factor; induced | 2.50 | – |

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| YNL333W | *SNZ2* | Member of a stationary phase-induced gene family; transcription of SNZ2 is induced prior to diauxic shift, and also in the absence of thiamin in a Thi2p- | 2.50 | 2.15 |
| YIR033W | *MGA2* | ER membrane protein involved in regulation of OLE1 transcription, acts with homolog Spt23p; inactive ER form dimerizes and one subunit is then activated by | 2.48 | 2.54 |
| YMR116C | *ASC1* | G-protein beta subunit and guanine nucleotide dissociation inhibitor for Gpa2p; ortholog of RACK1 that inhibits translation; core component of the small | 2.48 | 2.55 |
| YER070W | *RNR1* | Major isoform of the large subunit of ribonucleotide-diphosphate reductase; the RNR complex catalyzes rate-limiting step in dNTP synthesis, regulated by | 2.47 | 7.99 |
| YAR018C | *KIN3* | Nonessential protein kinase with unknown cellular | 2.46 | – |
| YDR507C | *GIN4* | Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; | 2.46 | – |
| YBR071W | *YBR071W* | Putative protein of unknown function; (GFP)-fusion and epitope-tagged proteins localize to the | 2.46 | – |
| YEL040W | *UTR2* | Chitin transglycosylase that functions in the transfer of chitin to beta(1-6) and beta(1-3) glucans in the cell wall; similar to and functionally redundant with Crh1; | 2.46 | – |
| YFL037W | *TUB2* | Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes | 2.46 | 2.34 |
| YML085C | *TUB1* | Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form | 2.45 | 2.30 |
| YBL063W | *KIP1* | Kinesin-related motor protein required for mitotic spindle assembly, chromosome segregation, and 2 micron plasmid partitioning; functionally redundant | 2.44 | – |
| YPL163C | *SVS1* | Cell wall and vacuolar protein, required for wild-type | 2.43 | – |
| YOR025W | *HST3* | Member of the Sir2 family of NAD(+)-dependent protein deacetylases; involved along with Hst4p in telomeric silencing, cell cycle progression, radiation | 2.43 | – |
| YNL135C | *FPR1* | Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and | 2.43 | 2.31 |
| YJR118C | *ILM1* | Protein of unknown function; may be involved in mitochondrial DNA maintenance; required for slowed | 2.41 | 2.05 |
| YML028W | *TSA1* | Thioredoxin peroxidase, acts as both a ribosome-associated and free cytoplasmic antioxidant; self-associates to form a high-molecular weight | 2.41 | 3.43 |
| YJL045W | *YJL045W* | Minor succinate dehydrogenase isozyme; homologous to Sdh1p, the major isozyme reponsible for the oxidation of succinate and transfer of | 2.40 | – |

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|---|---|---|---|---|
| YKL107W | *YKL107W* | Putative protein of unknown function; proposed to | 2.38 | 2.30 |
| YLR413W | *YLR413W* | Putative protein of unknown function; YLR413W is | 2.38 | 4.85 |
| YDR113C | *PDS1* | Securin, inhibits anaphase by binding separin Esp1p; blocks cyclin destruction and mitotic exit, essential for meiotic progression and mitotic cell cycle arrest; | 2.36 | – |
| YNL067W | *RPL9B* | Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl9Ap and has similarity | 2.35 | – |
| YPL255W | *BBP1* | Protein required for the spindle pole body (SPB) duplication, localized at the central plaque periphery; forms a complex with a nuclear envelope protein | 2.35 | 2.17 |
| YGL242C | *YGL242C* | Putative protein of unknown function; deletion | 2.35 | 4.01 |
| YJR047C | *ANB1* | Translation elongation factor eIF-5A, previously thought to function in translation initiation; similar to and functionally redundant with Hyp2p; undergoes | 2.33 | – |
| YAL024C | *LTE1* | Protein similar to GDP/GTP exchange factors but without detectable GEF activity; required for asymmetric localization of Bfa1p at daughter-directed | 2.32 | – |
| YBR160W | *CDC28* | Catalytic subunit of the main cell cycle cyclin-dependent kinase (CDK); alternately associates with | 2.31 | 2.15 |
| YMR179W | *SPT21* | Protein with a role in transcriptional silencing; required for normal transcription at several loci including HTA2-HTB2 and HHF2-HHT2, but not | 2.30 | – |
| YKL165C | *MCD4* | Protein involved in glycosylphosphatidylinositol (GPI) anchor synthesis; multimembrane-spanning protein that localizes to the endoplasmic reticulum; highly | 2.30 | 6.19 |
| YLL002W | *RTT109* | Histone acetyltransferase critical for cell survival in the presence of DNA damage during S phase; acetylates H3-K56 and H3-K9; involved in non- | 2.30 | – |
| YJL091C | *GWT1* | Protein involved in the inositol acylation of glucosaminyl phosphatidylinositol (GlcN-PI) to form glucosaminyl(acyl)phosphatidylinositol (GlcN(acyl)PI), | 2.30 | 3.32 |
| YML058W | *SML1* | Ribonucleotide reductase inhibitor involved in regulating dNTP production; regulated by Mec1p and | 2.29 | 2.11 |
| YKR042W | *UTH1* | Mitochondrial outer membrane and cell wall localized SUN family member involved in cell wall biogenesis and required for mitochondrial autophagy; | 2.29 | – |
| YBL035C | *POL12* | B subunit of DNA polymerase alpha-primase complex, required for initiation of DNA replication during mitotic and premeiotic DNA synthesis; also functions | 2.29 | – |
| YMR001C | *CDC5* | Polo-like kinase with multiple functions in mitosis and cytokinesis through substrate phosphorylation, also functions in adaptation to DNA damage during | 2.27 | – |

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| YLR273C | *PIG1* | Putative targeting subunit for the type-1 protein phosphatase Glc7p that tethers it to the Gsy2p | 2.27 | – |
| YHR061C | *GIC1* | Protein of unknown function involved in initiation of budding and cellular polarization, interacts with | 2.26 | – |
| YGR260W | *TNA1* | High affinity nicotinic acid plasma membrane permease, responsible for uptake of low levels of nicotinic acid; expression of the gene increases in the | 2.26 | – |
| YGR014W | *MSB2* | Mucin family member involved in the Cdc42p- and MAP kinase-dependent filamentous growth signaling pathway; also functions as an osmosensor in parallel | 2.24 | – |
| YJL219W | *HXT9* | Putative hexose transporter that is nearly identical to Hxt11p, has similarity to major facilitator superfamily (MFS) transporters, expression of HXT9 is regulated | 2.24 | – |
| YOR071C | *NRT1* | High-affinity nicotinamide riboside transporter; also transports thiamine with low affinity; shares sequence similarity with Thi7p and Thi72p; proposed | 2.21 | – |
| YAR008W | *SEN34* | Subunit of the tRNA splicing endonuclease, which is composed of Sen2p, Sen15p, Sen34p, and Sen54p; Sen34p contains the active site for tRNA 3' splice site | 2.21 | 2.59 |
| YGR254W | *ENO1* | Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the | 2.20 | 2.67 |
| YDR368W | *YPR1* | NADPH-dependent aldo-keto reductase, reduces multiple substrates including 2-methylbutyraldehyde and D,L-glyceraldehyde, expression is induced by | 2.20 | 2.25 |
| YGL038C | *OCH1* | Mannosyltransferase of the cis-Golgi apparatus, initiates the polymannose outer chain elongation of N- | 2.19 | – |
| YOL120C | *RPL18A* | Protein component of the large (60S) ribosomal subunit, identical to Rpl18Bp and has similarity to rat L18 ribosomal protein; intron of RPL18A pre-mRNA | 2.19 | – |
| YNL012W | *SPO1* | Meiosis-specific prospore protein; required for meiotic spindle pole body duplication and separation; required to produce bending force necessary for | 2.19 | – |
| YLR231C | *BNA5* | Kynureninase, required for the de novo biosynthesis of NAD from tryptophan via kynurenine; expression | 2.19 | 2.41 |
| YGR049W | *SCM4* | Potential regulatory effector of CDC4 function, suppresses a temperature-sensitive allele of CDC4, tripartite protein structure in which a charged region | 2.19 | – |
| YPR175W | *DPB2* | Second largest subunit of DNA polymerase II (DNA polymerase epsilon), required for normal yeast chromosomal replication; expression peaks at the | 2.18 | – |

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| YHR043C | *DOG2* | 2-deoxyglucose-6-phosphate phosphatase, member of a family of low molecular weight phosphatases, similar to Dog1p, induced by oxidative and osmotic | 2.18 | 3.70 |
| YGR037C | *ACB1* | Acyl-CoA-binding protein, transports newly synthesized acyl-CoA esters from fatty acid synthetase (Fas1p-Fas2p) to acyl-CoA-consuming | 2.16 | 2.74 |
| YER154W | *OXA1* | Mitochondrial inner membrane insertase, mediates the insertion of both mitochondrial- and nuclear-encoded proteins from the matrix into the inner | 2.16 | – |
| YJL115W | *ASF1* | Nucleosome assembly factor, involved in chromatin assembly and disassembly, anti-silencing protein that causes derepression of silent loci when | 2.15 | – |
| YDL164C | *CDC9* | DNA ligase found in the nucleus and mitochondria, an essential enzyme that joins Okazaki fragments during DNA replication; also acts in nucleotide excision | 2.15 | – |
| YPL158C | *AIM44* | Protein of unknown function; GFP-fusion protein localizes to the bud neck; transcription is regulated by | 2.14 | – |
| YGL226C-A | *OST5* | Zeta subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine- | 2.14 | 2.22 |
| YBR243C | *ALG7* | UDP-N-acetyl-glucosamine-1-P transferase, transfers Glc-Nac-P from UDP-GlcNac to Dol-P in the ER in the first step of the dolichol pathway of protein | 2.14 | – |
| YMR198W | *CIK1* | Kinesin-associated protein required for both karyogamy and mitotic spindle organization, interacts stably and specifically with Kar3p and may function to | 2.14 | – |
| YDR309C | *GIC2* | Redundant rho-like GTPase Cdc42p effector; homolog of Gic1p; involved in initiation of budding and cellular polarization; interacts with Cdc42p via the Cdc42/Rac- | 2.14 | – |
| YLR187W | *SKG3* | Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; potential | 2.14 | – |
| YKR010C | *TOF2* | Protein required for rDNA silencing and mitotic rDNA condensation; stimulates Cdc14p phosphatase activity and biphasic release to promote rDNA repeat | 2.13 | – |
| YDR009W | *GAL3* | Transcriptional regulator involved in activation of the GAL genes in response to galactose; forms a complex with Gal80p to relieve Gal80p inhibition of Gal4p; | 2.12 | – |
| YPL227C | *ALG5* | UDP-glucose:dolichyl-phosphate glucosyltransferase, involved in asparagine-linked glycosylation in the | 2.11 | – |
| YGR156W | *PTI1* | Essential protein that is a component of CPF (cleavage and polyadenylation factor); involved in 3' end formation of snoRNA and mRNA; interacts | 2.11 | – |

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| YML078W | *CPR3* | Mitochondrial peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; | 2.11 | – |
| YNL246W | *VPS75* | NAP family histone chaperone; binds to histones and Rtt109p, stimulating histone acetyltransferase activity; possesses nucleosome assembly activity in | 2.10 | – |
| YLR084C | *RAX2* | N-glycosylated protein involved in the maintenance of bud site selection during bipolar budding; | 2.10 | – |
| YLR209C | *PNP1* | Purine nucleoside phosphorylase, specifically metabolizes inosine and guanosine nucleosides; | 2.09 | – |
| YOL143C | *RIB4* | Lumazine synthase (6,7-dimethyl-8-ribityllumazine synthase, also known as DMRL synthase); catalyzes | 2.07 | 3.24 |
| YJL181W | *YJL181W* | Putative protein of unknown function; expression is cell-cycle regulated as shown by microarray analysis | 2.07 | – |
| YLR134W | *PDC5* | Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde, regulation is glucose- and | 2.07 | 3.16 |
| YGR292W | *MAL12* | Maltase (alpha-D-glucosidase), inducible protein involved in maltose catabolism; encoded in the MAL1 complex locus; hydrolyzes the disaccharides maltose, | 2.07 | – |
| YAL062W | *GDH3* | NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization | 2.06 | 2.11 |
| YFL045C | *SEC53* | Phosphomannomutase, involved in synthesis of GDP-mannose and dolichol-phosphate-mannose; required | 2.06 | – |
| YDR261C | *EXG2* | Exo-1,3-beta-glucanase, involved in cell wall beta-glucan assembly; may be anchored to the plasma | 2.04 | – |
| YKL113C | *RAD27* | 5' to 3' exonuclease, 5' flap endonuclease, required for Okazaki fragment processing and maturation as well as for long-patch base-excision repair; member | 2.04 | – |
| YLR293C | *GSP1* | Ran GTPase, GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; | 2.04 | 2.36 |
| YNL072W | *RNH201* | Ribonuclease H2 catalytic subunit, removes RNA primers during Okazaki fragment synthesis and errant ribonucleotides misincorporated during DNA | 2.03 | 2.49 |
| YHR149C | *SKG6* | Integral membrane protein that localizes primarily to growing sites such as the bud tip or the cell | 2.03 | – |
| YPL208W | *RKM1* | SET-domain lysine-N-methyltransferase, catalyzes the formation of dimethyllysine residues on the large | 2.03 | – |
| YGL251C | *HFM1* | Meiosis specific DNA helicase involved in the conversion of double-stranded breaks to later recombination intermediates and in crossover | 2.03 | – |

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| YDL145C | *COP1* | Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles in the early | 2.02 | 2.15 |
| YGR221C | *TOS2* | Protein involved in localization of Cdc24p to the site of bud growth; may act as a membrane anchor; | 2.02 | 2.09 |
| YML009C | *MRPL39* | Mitochondrial ribosomal protein of the large subunit | 2.01 | – |
| YJR048W | *CYC1* | Cytochrome c, isoform 1; electron carrier of the mitochondrial intermembrane space that transfers electrons from ubiquinone-cytochrome c | 2.00 | 3.06 |
| YLR272C | *YCS4* | Subunit of the condensin complex; required for establishment and maintenance of chromosome condensation, chromosome segregation, chromatin | 2.00 | – |
| YDR361C | *BCP1* | Essential protein involved in nuclear export of Mss4p, which is a lipid kinase that generates phosphatidylinositol 4,5-biphosphate and plays a role | -2.01 | – |
| YML099C | *ARG81* | Zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type, involved in the | -2.01 | – |
| YGR030C | *POP6* | Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors | -2.01 | – |
| YLL056C | *YLL056C* | Putative protein of unknown function, transcription is activated by paralogous transcription factors Yrm1p and Yrr1p and genes involved in pleiotropic drug | -2.02 | – |
| YPR086W | *SUA7* | Transcription factor TFIIB, a general transcription factor required for transcription initiation and start | -2.02 | -2.18 |
| YDL169C | *UGX2* | Protein of unknown function, transcript accumulates in response to any combination of stress conditions | -2.02 | – |
| YBR293W | *VBA2* | Permease of basic amino acids in the vacuolar | -2.03 | -2.58 |
| YDR465C | *RMT2* | Arginine N5 methyltransferase; methylates ribosomal | -2.04 | – |
| YNL314W | *DAL82* | Positive regulator of allophanate inducible genes; binds a dodecanucleotide sequence upstream of all genes that are induced by allophanate; contains an | -2.04 | – |
| YDL025C | *YDL025C* | Putative protein kinase, potentially phosphorylated by Cdc28p; interacts with ribosome biogenesis | -2.04 | – |
| YPR157W | *YPR157W* | Putative protein of unknown function; induced by treatment with 8-methoxypsoralen and UVA | -2.05 | – |
| YPL199C | *YPL199C* | Putative protein of unknown function, predicted to | -2.06 | -2.56 |
| YDR244W | *PEX5* | Peroxisomal membrane signal receptor for the C-terminal tripeptide signal sequence (PTS1) of peroxisomal matrix proteins, required for | -2.07 | – |
| YNL004W | *HRB1* | Poly(A+) RNA-binding protein, involved in the export of mRNAs from the nucleus to the cytoplasm; similar | -2.07 | -2.15 |
| YBR297W | *MAL33* | MAL-activator protein, part of complex locus MAL3; nonfunctional in genomic reference strain S288C | -2.07 | – |

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| YHR066W | *SSF1* | Constituent of 66S pre-ribosomal particles, required for ribosomal large subunit maturation; functionally | -2.07 | -4.63 |
| YMR265C | *YMR265C* | Putative protein of unknown function | -2.08 | -2.35 |
| YDL121C | *YDL121C* | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to | -2.08 | -2.47 |
| YPR112C | *MRD1* | Essential conserved protein that is part of the 90S preribosome; required for production of 18S rRNA | -2.08 | – |
| YNL119W | *NCS2* | Protein required for thiolation of the uridine at the wobble position of Lys(UUU) and Glu(UUC) tRNAs; has a role in urmylation and in invasive and | -2.11 | – |
| YOR213C | *SAS5* | Subunit of the SAS complex (Sas2p, Sas4p, Sas5p), which acetylates free histones and nucleosomes and | -2.11 | – |
| YER015W | *FAA2* | Medium chain fatty acyl-CoA synthetase, activates imported fatty acids; accepts a wide range of fatty acid chain lengths with a preference for medium | -2.11 | -2.09 |
| YOR179C | *SYC1* | Subunit of the APT subcomplex of cleavage and polyadenylation factor, may have a role in 3' end | -2.11 | – |
| YLR161W | *YLR161W* | Putative protein of unknown function; YLR156W, YLR159W, and YLR161W are three identical open | -2.11 | – |
| YPR048W | *TAH18* | Conserved NAPDH-dependent diflavin reductase, component of an early step in the cytosolic Fe-S protein assembly (CIA) machinery; transfers electrons | -2.11 | – |
| YDR312W | *SSF2* | Protein required for ribosomal large subunit maturation, functionally redundant with Ssf1p; | -2.11 | – |
| YHR166C | *CDC23* | Subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase | -2.13 | -2.12 |
| YOL136C | *PFK27* | 6-phosphofructo-2-kinase, catalyzes synthesis of fructose-2,6-bisphosphate; inhibited by phosphoenolpyruvate and sn-glycerol 3-phosphate, | -2.14 | – |
| YOR101W | *RAS1* | GTPase involved in G-protein signaling in the adenylate cyclase activating pathway, plays a role in cell proliferation; localized to the plasma membrane; | -2.14 | – |
| YDL223C | *HBT1* | Substrate of the Hub1p ubiquitin-like protein that localizes to the shmoo tip (mating projection); mutants are defective for mating projection | -2.14 | – |
| YNL113W | *RPC19* | RNA polymerase subunit AC19, common to RNA | -2.14 | – |
| YKL099C | *UTP11* | Subunit of U3-containing Small Subunit (SSU) processome complex involved in production of 18S | -2.15 | – |
| YGL153W | *PEX14* | Peroxisomal membrane peroxin that is a central component of the peroxisomal protein import machinery; interacts with both PTS1 (Pex5p) and | -2.15 | – |

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| YJL212C | *OPT1* | Proton-coupled oligopeptide transporter of the plasma membrane; also transports glutathione and | -2.16 | -3.25 |
| YLR407W | *YLR407W* | Putative protein of unknown function; null mutant displays elongated buds and a large fraction of | -2.18 | – |
| YLR159W | *YLR159W* | Putative protein of unknown function; YLR156W, YLR159W, and YLR161W are three identical open | -2.18 | – |
| YKR058W | *GLG1* | Self-glucosylating initiator of glycogen synthesis, also glucosylates n-dodecyl-beta-D-maltoside; similar to | -2.18 | – |
| YJL112W | *MDV1* | Peripheral protein of the cytosolic face of the mitochondrial outer membrane, required for mitochondrial fission; interacts with Fis1p and with | -2.19 | – |
| YCR100C | *YCR100C* | Putative protein of unknown function | -2.19 | -2.34 |
| YLL051C | *FRE6* | Putative ferric reductase with similarity to Fre2p; | -2.19 | – |
| YGR202C | *PCT1* | Cholinephosphate cytidylyltransferase, also known as CTP:phosphocholine cytidylyltransferase, rate-determining enzyme of the CDP-choline pathway for | -2.20 | – |
| YDR030C | *RAD28* | Protein involved in DNA repair, related to the human CSA protein that is involved in transcription-coupled | -2.20 | – |
| YGR081C | *SLX9* | Protein required for pre-rRNA processing; associated with the 90S pre-ribosome and 43S small ribosomal subunit precursor; interacts with U3 snoRNA; | -2.20 | -2.57 |
| YIL113W | *SDP1* | Stress-inducible dual-specificity MAP kinase phosphatase, negatively regulates Slt2p MAP kinase by direct dephosphorylation, diffuse localization | -2.20 | – |
| YPL202C | *AFT2* | Iron-regulated transcriptional activator; activates genes involved in intracellular iron use and required | -2.21 | – |
| YER037W | *PHM8* | Protein of unknown function, expression is induced by low phosphate levels and by inactivation of | -2.22 | – |
| YBL033C | *RIB1* | GTP cyclohydrolase II; catalyzes the first step of the | -2.22 | -2.34 |
| YGR129W | *SYF2* | Member of the NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of the spliceosome containing U2, U5, and U6 | -2.22 | – |
| YOR056C | *NOB1* | Essential nuclear protein involved in proteasome maturation and synthesis of 40S ribosomal subunits; | -2.23 | – |
| YOR262W | *YOR262W* | Protein of unknown function required for establishment of sister chromatid cohesion; contains an ATP/GTP binding site motif; similar to YLR243W | -2.23 | – |
| YPL212C | *PUS1* | tRNA:pseudouridine synthase, introduces pseudouridines at positions 26-28, 34-36, 65, and 67 | -2.24 | – |
| YMR185W | *YMR185W* | Putative protein of unknown function; conflicting evidence on whether null mutant is viable with | -2.25 | – |
| YER184C | *YER184C* | Putative zinc cluster protein; deletion confers sensitivity to Calcufluor white, and prevents growth | -2.25 | -3.03 |

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| YIR031C | *DAL7* | Malate synthase, role in allantoin degradation unknown; expression sensitive to nitrogen catabolite | -2.26 | – |
| YJL072C | *PSF2* | Subunit of the GINS complex (Sld5p, Psf1p, Psf2p, Psf3p), which is localized to DNA replication origins | -2.26 | -3.81 |
| YKL106W | *AAT1* | Mitochondrial aspartate aminotransferase, catalyzes the conversion of oxaloacetate to aspartate in | -2.26 | – |
| YBR141C | *YBR141C* | Putative S-adenosylmethionine-dependent methyltransferase; green fluorescent protein (GFP)- | -2.26 | – |
| YNL221C | *POP1* | Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors | -2.29 | -2.07 |
| YOR004W | *UTP23* | Essential nucleolar protein that is a component of the SSU (small subunit) processome involved in 40S ribosomal subunit biogenesis; has homology to PINc | -2.30 | -2.09 |
| YHR150W | *PEX28* | Peroxisomal integral membrane peroxin, involved in the regulation of peroxisomal size, number and distribution; genetic interactions suggest that Pex28p | -2.30 | – |
| YKR024C | *DBP7* | Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; essential | -2.31 | – |
| YLR284C | *ECI1* | Peroxisomal delta3,delta2-enoyl-CoA isomerase, hexameric protein that converts 3-hexenoyl-CoA to trans-2-hexenoyl-CoA, essential for the beta- | -2.32 | – |
| YDR421W | *ARO80* | Zinc finger transcriptional activator of the Zn2Cys6 family; activates transcription of aromatic amino acid | -2.32 | – |
| YER137C | *YER137C* | Putative protein of unknown function | -2.35 | – |
| YOR338W | *YOR338W* | Putative protein of unknown function; YOR338W transcription is regulated by Azf1p and its transcript is a specific target of the G protein effector Scp160p; | -2.35 | – |
| YCR107W | *AAD3* | Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase; | -2.35 | – |
| YMR201C | *RAD14* | Protein that recognizes and binds damaged DNA during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 1 (NEF1); contains | -2.37 | – |
| YBL054W | *TOD6* | PAC motif binding protein involved in rRNA and ribosome biogenesis; subunit of the RPD3L histone deacetylase complex; Myb-like HTH transcription | -2.37 | – |
| YBR257W | *POP4* | Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors | -2.38 | -2.59 |
| YBR105C | *VID24* | Peripheral membrane protein located at Vid (vacuole import and degradation) vesicles; regulates fructose-1,6-bisphosphatase (FBPase) targeting to the vacuole; | -2.39 | -3.67 |
| YKL072W | *STB6* | Protein that binds Sin3p in a two-hybrid assay | -2.39 | -2.55 |

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| YGR121C | *MEP1* | Ammonium permease; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport only ammonium (NH4+); expression is under the | -2.39 | -2.92 |
| YNL014W | *HEF3* | Translational elongation factor EF-3; paralog of YEF3 and member of the ABC superfamily; stimulates EF-1 alpha-dependent binding of aminoacyl-tRNA by the | -2.40 | – |
| YPL230W | *USV1* | Putative transcription factor containing a C2H2 zinc finger; mutation affects transcriptional regulation of genes involved in growth on non-fermentable carbon | -2.40 | – |
| YLR312C | *YLR312C* | Putative protein of unknown function | -2.40 | -2.10 |
| YLR023C | *IZH3* | Membrane protein involved in zinc ion homeostasis, member of the four-protein IZH family, expression induced by zinc deficiency; deletion reduces | -2.42 | – |
| YMR009W | *ADI1* | Acireductone dioxygenease involved in the methionine salvage pathway; ortholog of human MTCBP-1; transcribed with YMR010W and regulated | -2.42 | – |
| YMR145C | *NDE1* | Mitochondrial external NADH dehydrogenase, a type II NAD(P)H:quinone oxidoreductase that catalyzes the oxidation of cytosolic NADH; Nde1p and Nde2p | -2.43 | – |
| YHR046C | *INM1* | Inositol monophosphatase, involved in biosynthesis of inositol and in phosphoinositide second messenger signaling; INM1 expression increases in the presence | -2.44 | -2.11 |
| YEL029C | *BUD16* | Putative pyridoxal kinase, a key enzyme involved in pyridoxal 5'-phosphate synthesis, the active form of vitamin B6; required for genome integrity; involved in | -2.44 | – |
| YFL030W | *AGX1* | Alanine:glyoxylate aminotransferase (AGT), catalyzes the synthesis of glycine from glyoxylate, which is one of three pathways for glycine biosynthesis in yeast; | -2.49 | -2.27 |
| YKL023W | *YKL023W* | Putative protein of unknown function, predicted by computational methods to be involved in mRNA | -2.50 | -3.03 |
| YOR192C | *THI72* | Transporter of thiamine or related compound; shares | -2.52 | -3.27 |
| YLR387C | *REH1* | Cytoplasmic 60S subunit biogenesis factor, associates with pre-60S particles; similar to Rei1p and shares partially redundant function in cytoplasmic 60S | -2.52 | – |
| YLL061W | *MMP1* | High-affinity S-methylmethionine permease, required for utilization of S-methylmethionine as a sulfur | -2.53 | – |
| YBL069W | *AST1* | Peripheral membrane protein that interacts with the plasma membrane ATPase Pma1p and has a role in its targeting to the plasma membrane, possibly by | -2.54 | – |
| YPL017C | *IRC15* | Microtubule associated protein; regulates microtubule dynamics; required for accurate meiotic chromosome segregation; null mutant displays large | -2.56 | -2.27 |

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| YNL234W | *YNL234W* | Protein of unknown function with similarity to globins; has a functional heme-binding domain; mutant has aneuploidy tolerance; transcription | -2.57 | – |
| YOL165C | *AAD15* | Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase; | -2.60 | -2.72 |
| YGR159C | *NSR1* | Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and | -2.61 | – |
| YDR120C | *TRM1* | tRNA methyltransferase; two forms of the protein are made by alternative translation starts; localizes to both the nucleus and mitochondrion to produce the | -2.65 | – |
| YKL143W | *LTV1* | Component of the GSE complex, which is required for proper sorting of amino acid permease Gap1p; required for ribosomal small subunit export from | -2.68 | – |
| YLR460C | *YLR460C* | Member of the quinone oxidoreductase family, up-regulated in response to the fungicide mancozeb; | -2.71 | – |
| YPR111W | *DBF20* | Ser/Thr kinase involved in late nuclear division, one of the mitotic exit network (MEN) proteins; necessary | -2.73 | -3.36 |
| YHR088W | *RPF1* | Nucleolar protein involved in the assembly and export of the large ribosomal subunit; constituent of 66S pre-ribosomal particles; contains a sigma(70)-like | -2.76 | -2.13 |
| YLL053C | *YLL053C* | Putative protein; in the Sigma 1278B strain background YLL053C is contiguous with AQY2 which | -2.79 | -2.85 |
| YDR342C | *HXT7* | High-affinity glucose transporter of the major facilitator superfamily, nearly identical to Hxt6p, expressed at high basal levels relative to other HXTs, | -2.80 | – |
| YFL061W | *DDI2* | Protein of unknown function; expression is induced over 100-fold by DNA damage; induction decreased | -2.87 | -5.18 |
| YLR297W | *YLR297W* | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; YLR297W is not an essential gene; | -2.88 | – |
| YLL052C | *AQY2* | Water channel that mediates the transport of water across cell membranes, only expressed in proliferating cells, controlled by osmotic signals, may | -2.89 | -3.13 |
| YOR363C | *PIP2* | Autoregulatory oleate-specific transcriptional activator of peroxisome proliferation, contains Zn(2)-Cys(6) cluster domain, forms heterodimer with | -2.90 | – |
| YMR189W | *GCV2* | P subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels | -2.90 | -5.24 |
| YKR099W | *BAS1* | Myb-related transcription factor involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways; also | -2.91 | -4.06 |
| YIL019W | *FAF1* | Protein required for pre-rRNA processing and 40S | -2.94 | – |

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| YHR033W | *YHR033W* | Putative protein of unknown function; epitope- | -2.95 | – |
| YGR239C | *PEX21* | Peroxin required for targeting of peroxisomal matrix proteins containing PTS2; interacts with Pex7p; | -3.02 | -4.21 |
| YDR343C | *HXT6* | High-affinity glucose transporter of the major facilitator superfamily, nearly identical to Hxt7p, expressed at high basal levels relative to other HXTs, | -3.02 | – |
| YLR152C | *YLR152C* | Putative protein of unknown function; YLR152C is not | -3.03 | -4.74 |
| YIL003W | *CFD1* | Highly conserved, iron-sulfur cluster binding protein localized in the cytoplasm; forms a complex with | -3.03 | -3.22 |
| YDR533C | *HSP31* | Possible chaperone and cysteine protease with similarity to E. coli Hsp31; member of the DJ-1/ThiJ/PfpI superfamily, which includes human DJ-1 | -3.03 | -2.24 |
| YER176W | *ECM32* | DNA dependent ATPase/DNA helicase belonging to the Dna2p- and Nam7p-like family of helicases that is involved in modulating translation termination; | -3.05 | – |
| YDL170W | *UGA3* | Transcriptional activator necessary for gamma-aminobutyrate (GABA)-dependent induction of GABA genes (such as UGA1, UGA2, UGA4); zinc-finger | -3.18 | -5.69 |
| YOL158C | *ENB1* | Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated | -3.21 | -3.60 |
| YDR019C | *GCV1* | T subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels | -3.24 | -4.41 |
| YNL162W-A | *YNL162W-A* | Putative protein of unknown function; identified by | -3.25 | – |
| YNL279W | *PRM1* | Pheromone-regulated multispanning membrane protein involved in membrane fusion during mating; predicted to have 5 transmembrane segments and a | -3.29 | – |
| YKL155C | *RSM22* | Mitochondrial ribosomal protein of the small subunit; also predicted to be an S-adenosylmethionine- | -3.63 | – |
| YER145C | *FTR1* | High affinity iron permease involved in the transport of iron across the plasma membrane; forms complex | -3.64 | -5.70 |
| YNL142W | *MEP2* | Ammonium permease involved in regulation of pseudohyphal growth; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport | -3.66 | – |
| YMR107W | *SPG4* | Protein required for survival at high temperature during stationary phase; not required for growth on | -4.07 | – |
| YOR306C | *MCH5* | Plasma membrane riboflavin transporter; facilitates the uptake of vitamin B2; required for FAD-dependent processes; sequence similarity to | -4.11 | – |
| YML123C | *PHO84* | High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to | -4.19 | – |

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| YNL112W | *DBP2* | Essential ATP-dependent RNA helicase of the DEAD-box protein family, involved in nonsense-mediated | -4.19 | – |
| YNR069C | *BSC5* | Protein of unknown function, ORF exhibits genomic organization compatible with a translational | -4.47 | – |
| YJL213W | *YJL213W* | Protein of unknown function that may interact with ribosomes; periodically expressed during the yeast metabolic cycle; phosphorylated in vitro by the | -4.50 | -13.17 |
| YPL092W | *SSU1* | Plasma membrane sulfite pump involved in sulfite metabolism and required for efficient sulfite efflux; | -4.79 | -6.75 |
| YGR230W | *BNS1* | Protein with some similarity to Spo12p; overexpression bypasses need for Spo12p, but not | -4.87 | -3.61 |
| YIR032C | *DAL3* | Ureidoglycolate hydrolase, converts ureidoglycolate to glyoxylate and urea in the third step of allantoin | -5.20 | -4.19 |
| YPR192W | *AQY1* | Spore-specific water channel that mediates the transport of water across cell membranes, developmentally controlled; may play a role in spore | -5.28 | – |
| YHR048W | *YHK8* | Presumed antiporter of the DHA1 family of multidrug resistance transporters; contains 12 predicted transmembrane spans; expression of gene is up- | -5.55 | -6.38 |
| YLL055W | *YCT1* | High-affinity cysteine-specific transporter with similarity to the Dal5p family of transporters; green fluorescent protein (GFP)-fusion protein localizes to | -5.99 | – |
| YIL165C | *YIL165C* | Putative protein of unknown function; mutant exhibits mitophagy defects; in closely related species and other S. cerevisiae strain backgrounds YIL165C | -6.03 | -7.59 |
| YIL164C | *NIT1* | Nitrilase, member of the nitrilase branch of the nitrilase superfamily; in closely related species and other S. cerevisiae strain backgrounds YIL164C and | -6.31 | -7.94 |
| YOR186W | *YOR186W* | Putative protein of unknown function; proper regulation of expression during heat stress is | -6.37 | -6.03 |
| YMR058W | *FET3* | Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to | -6.64 | -11.97 |
| YFR055W | *IRC7* | Putative cystathionine beta-lyase; involved in copper ion homeostasis and sulfur metabolism; null mutant displays increased levels of spontaneous Rad52p foci; | -6.82 | -11.69 |
| YDR242W | *AMD2* | Putative amidase | -7.12 | -8.88 |
| YBL043W | *ECM13* | Non-essential protein of unknown function; induced by treatment with 8-methoxypsoralen and UVA | -7.22 | -9.22 |
| YHL016C | *DUR3* | Plasma membrane transporter for both urea and polyamines, expression is highly sensitive to nitrogen catabolite repression and induced by allophanate, the | -7.66 | -8.79 |

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| YPL095C | *EEB1* | Acyl-coenzymeA:ethanol O-acyltransferase responsible for the major part of medium-chain fatty acid ethyl ester biosynthesis during fermentation; | -8.32 | -3.60 |
| YCL064C | *CHA1* | Catabolic L-serine (L-threonine) deaminase, catalyzes the degradation of both L-serine and L-threonine; required to use serine or threonine as the sole | -9.36 | -12.61 |
| YHR096C | *HXT5* | Hexose transporter with moderate affinity for glucose, induced in the presence of non-fermentable carbon sources, induced by a decrease in growth | -9.51 | -8.23 |
| YHR137W | *ARO9* | Aromatic aminotransferase II, catalyzes the first step of tryptophan, phenylalanine, and tyrosine | -16.37 | -10.86 |
| YKR034W | *DAL80* | Negative regulator of genes in multiple nitrogen degradation pathways; expression is regulated by nitrogen levels and by Gln3p; member of the GATA- | -22.06 | – |
| YJL153C | *INO1* | Inositol-3-phosphate synthase, involved in synthesis of inositol phosphates and inositol-containing phospholipids; transcription is coregulated with other | – | 32.84 |
| YER003C | *PMI40* | Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and mannose-6-P; | – | 8.04 |
| YGR109C | *CLB6* | B-type cyclin involved in DNA replication during S phase; activates Cdc28p to promote initiation of DNA synthesis; functions in formation of mitotic spindles | – | 6.29 |
| YKL165C | *MCD4* | Protein involved in glycosylphosphatidylinositol (GPI) anchor synthesis; multimembrane-spanning protein that localizes to the endoplasmic reticulum; highly | – | 6.19 |
| YGR256W | *GND2* | 6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating | – | 6.06 |
| YOR387C | *YOR387C* | Putative protein of unknown function; regulated by the metal-responsive Aft1p transcription factor; | – | 5.85 |
| YBR088C | *POL30* | Proliferating cell nuclear antigen (PCNA), functions as the sliding clamp for DNA polymerase delta; may function as a docking site for other proteins required | – | 5.26 |
| YML058W-A | *HUG1* | Protein involved in the Mec1p-mediated checkpoint pathway that responds to DNA damage or replication | – | 5.03 |
| YGR213C | *RTA1* | Protein involved in 7-aminocholesterol resistance; has seven potential membrane-spanning regions; expression is induced under both low-heme and low- | – | 4.73 |
| YNR016C | *ACC1* | Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form | – | 4.40 |
| YLR099C | *ICT1* | Lysophosphatidic acid acyltransferase, responsible for enhanced phospholipid synthesis during organic solvent stress; null displays increased sensitivity to | – | 4.32 |

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| YGL253W | *HXK2* | Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; predominant hexokinase during growth on glucose; | − | 4.18 |
| YGR234W | *YHB1* | Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in | − | 3.97 |
| YAL023C | *PMT2* | Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein Ser/Thr residues; involved in ER quality | − | 3.84 |
| YML070W | *DAK1* | Dihydroxyacetone kinase, required for detoxification of dihydroxyacetone (DHA); involved in stress | − | 3.75 |
| YOR388C | *FDH1* | NAD(+)-dependent formate dehydrogenase, may | − | 3.45 |
| YML028W | *TSA1* | Thioredoxin peroxidase, acts as both a ribosome-associated and free cytoplasmic antioxidant; self-associates to form a high-molecular weight | − | 3.43 |
| YKL182W | *FAS1* | Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl | − | 3.41 |
| YJL167W | *ERG20* | Farnesyl pyrophosphate synthetase, has both dimethylallyltranstransferase and geranyltranstransferase activities; catalyzes the | − | 3.41 |
| YOL143C | *RIB4* | Lumazine synthase (6,7-dimethyl-8-ribityllumazine synthase, also known as DMRL synthase); catalyzes | − | 3.24 |
| YHR174W | *ENO2* | Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the | − | 3.20 |
| YLR134W | *PDC5* | Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde, regulation is glucose- and | − | 3.16 |
| YOR321W | *PMT3* | Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts in a complex | − | 3.15 |
| YHR183W | *GND1* | 6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required | − | 3.13 |
| YLR354C | *TAL1* | Transaldolase, enzyme in the non-oxidative pentose phosphate pathway; converts sedoheptulose 7-phosphate and glyceraldehyde 3-phosphate to | − | 3.10 |
| YOR198C | *BFR1* | Component of mRNP complexes associated with polyribosomes; implicated in secretion and nuclear | − | 3.03 |
| YOR393W | *ERR1* | Protein of unknown function, has similarity to | − | 3.02 |
| YFL011W | *HXT10* | Putative hexose transporter, expressed at low levels | − | 3.00 |
| YPL281C | *ERR2* | Protein of unknown function, has similarity to | − | 3.00 |
| YMR323W | *ERR3* | Protein of unknown function, has similarity to | − | 2.98 |

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| YOR288C | *MPD1* | Member of the protein disulfide isomerase (PDI) family; interacts with and inhibits the chaperone activity of Cne1p; MPD1 overexpression in a pdi1 null | – | 2.96 |
| YLR259C | *HSP60* | Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and | – | 2.81 |
| YMR214W | *SCJ1* | One of several homologs of bacterial chaperone DnaJ, located in the ER lumen where it cooperates | – | 2.76 |
| YPL240C | *HSP82* | Hsp90 chaperone required for pheromone signaling and negative regulation of Hsf1p; docks with Tom70p for mitochondrial preprotein delivery; promotes | – | 2.76 |
| YOR176W | *HEM15* | Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of ferrous iron into | – | 2.75 |
| YNR019W | *ARE2* | Acyl-CoA:sterol acyltransferase, isozyme of Are1p; endoplasmic reticulum enzyme that contributes the | – | 2.74 |
| YGR037C | *ACB1* | Acyl-CoA-binding protein, transports newly synthesized acyl-CoA esters from fatty acid synthetase (Fas1p-Fas2p) to acyl-CoA-consuming | – | 2.74 |
| YJR030C | *YJR030C* | Putative protein of unknown function; expression repressed in carbon limited vs carbon replete | – | 2.72 |
| YLR304C | *ACO1* | Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; | – | 2.72 |
| YOL031C | *SIL1* | Nucleotide exchange factor for the endoplasmic reticulum (ER) lumenal Hsp70 chaperone Kar2p, required for protein translocation into the ER; | – | 2.69 |
| YKL121W | *DGR2* | Protein of unknown function; null mutant is resistant to 2-deoxy-D-glucose and displays abnormally | – | 2.68 |
| YBR011C | *IPP1* | Cytoplasmic inorganic pyrophosphatase (PPase), homodimer that catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and | – | 2.67 |
| YBR029C | *CDS1* | Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + | – | 2.62 |
| YPL058C | *PDR12* | Plasma membrane ATP-binding cassette (ABC) transporter, weak-acid-inducible multidrug transporter required for weak organic acid resistance; | – | 2.60 |
| YNL102W | *POL1* | Catalytic subunit of the DNA polymerase I alpha-primase complex, required for the initiation of DNA | – | 2.60 |
| YLR234W | *TOP3* | DNA Topoisomerase III, conserved protein that functions in a complex with Sgs1p and Rmi1p to relax single-stranded negatively-supercoiled DNA | – | 2.56 |

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| YHR104W | *GRE3* | Aldose reductase involved in methylglyoxal, d-xylose, arabinose, and galactose metabolism; stress induced (osmotic, ionic, oxidative, heat shock, starvation and | – | 2.53 |
| YGL256W | *ADH4* | Alcohol dehydrogenase isoenzyme type IV, dimeric enzyme demonstrated to be zinc-dependent despite sequence similarity to iron-activated alcohol | – | 2.51 |
| YOR073W | *SGO1* | Component of the spindle checkpoint, involved in sensing lack of tension on mitotic chromosomes; protects centromeric Rec8p at meiosis I; required for | – | 2.51 |
| YDR148C | *KGD2* | Dihydrolipoyl transsuccinylase, component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes the oxidative | – | 2.49 |
| YKL103C | *LAP4* | Vacuolar aminopeptidase yscI; zinc metalloproteinase that belongs to the peptidase family M18; often used as a marker protein in studies of autophagy and | – | 2.48 |
| YOR247W | *SRL1* | Mannoprotein that exhibits a tight association with the cell wall, required for cell wall stability in the absence of GPI-anchored mannoproteins; has a high | – | 2.47 |
| YOR385W | *YOR385W* | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to | – | 2.43 |
| YOR254C | *SEC63* | Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP- | – | 2.42 |
| YDR050C | *TPI1* | Triose phosphate isomerase, abundant glycolytic enzyme; mRNA half-life is regulated by iron availability; transcription is controlled by activators | – | 2.41 |
| YCL050C | *APA1* | Diadenosine 5',5''-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase), involved in | – | 2.40 |
| YDL103C | *QRI1* | UDP-N-acetylglucosamine pyrophosphorylase, catalyzes the formation of UDP-N-acetylglucosamine (UDP-GlcNAc), which is important in cell wall | – | 2.38 |
| YDL022W | *GPD1* | NAD-dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression | – | 2.38 |
| YBL032W | *HEK2* | RNA binding protein involved in the asymmetric localization of ASH1 mRNA; represses translation of ASH1 mRNA, an effect reversed by Yck1p-dependent | – | 2.38 |
| YER103W | *SSA4* | Heat shock protein that is highly induced upon stress; plays a role in SRP-dependent cotranslational protein-membrane targeting and translocation; member of | – | 2.38 |
| YBR072W | *HSP26* | Small heat shock protein (sHSP) with chaperone activity; forms hollow, sphere-shaped oligomers that suppress unfolded proteins aggregation; oligomer | – | 2.37 |

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| YJR143C | *PMT4* | Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; appears to form | – | 2.37 |
| YGR285C | *ZUO1* | Ribosome-associated chaperone, functions in ribosome biogenesis and, in partnership with Ssz1p and SSb1/2, as a chaperone for nascent polypeptide | – | 2.36 |
| YGL137W | *SEC27* | Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective | – | 2.34 |
| YBL002W | *HTB2* | Histone H2B, core histone protein required for chromatin assembly and chromosome function; nearly identical to HTB1; Rad6p-Bre1p-Lge1p | – | 2.34 |
| YLR131C | *ACE2* | Transcription factor that activates expression of early G1-specific genes, localizes to daughter cell nuclei after cytokinesis and delays G1 progression in | – | 2.33 |
| YGR240C | *PFK1* | Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by | – | 2.33 |
| YKL152C | *GPM1* | Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2- | – | 2.29 |
| YLR132C | *YLR132C* | Essential protein of unknown function; fluorescent protein (GFP or YFP)-tagged protein localizes to | – | 2.28 |
| YNL082W | *PMS1* | ATP-binding protein required for mismatch repair in mitosis and meiosis; functions as a heterodimer with Mlh1p, binds double- and single-stranded DNA via its | – | 2.28 |
| YIL041W | *GVP36* | BAR domain-containing protein that localizes to both early and late Golgi vesicles; required for adaptation to varying nutrient concentrations, fluid-phase | – | 2.27 |
| YHR064C | *SSZ1* | Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome-associated complex that binds the ribosome via the Zuo1p subunit; also | – | 2.26 |
| YDR508C | *GNP1* | High-affinity glutamine permease, also transports Leu, Ser, Thr, Cys, Met and Asn; expression is fully dependent on Grr1p and modulated by the Ssy1p- | – | 2.26 |
| YFL059W | *SNZ3* | Member of a stationary phase-induced gene family; transcription of SNZ2 is induced prior to diauxic shift, and also in the absence of thiamin in a Thi2p- | – | 2.25 |
| YHL018W | *YHL018W* | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to | – | 2.24 |
| YOR083W | *WHI5* | Repressor of G1 transcription that binds to SCB binding factor (SBF) at SCB target promoters in early G1; phosphorylation of Whi5p by the CDK, | – | 2.20 |

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| YLR133W | *CKI1* | Choline kinase, catalyzing the first step in phosphatidylcholine synthesis via the CDP-choline (Kennedy pathway); exhibits some ethanolamine | – | 2.19 |
| YNL071W | *LAT1* | Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes | – | 2.19 |
| YDL004W | *ATP16* | Delta subunit of the central stalk of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily | – | 2.18 |
| YPR183W | *DPM1* | Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane, catalyzes the formation of Dol-P-Man from Dol-P and GDP-Man; required for glycosyl | – | 2.17 |
| YFL053W | *DAK2* | Dihydroxyacetone kinase, required for detoxification of dihydroxyacetone (DHA); involved in stress | – | 2.16 |
| YOR388C | *FDH1* | NAD(+)-dependent formate dehydrogenase, may | – | 2.16 |
| YDL192W | *ARF1* | ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated vesicle | – | 2.14 |
| YGL175C | *SAE2* | Endonuclease that processes hairpin DNA structures with the MRX complex; involved in meiotic and mitotic double-strand break repair; phosphorylated in | – | 2.14 |
| YBR053C | *YBR053C* | Putative protein of unknown function; induced by cell | – | 2.13 |
| YDL140C | *RPO21* | RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association | – | 2.12 |
| YDL219W | *DTD1* | D-Tyr-tRNA(Tyr) deacylase, functions in protein translation, may affect nonsense suppression via | – | 2.12 |
| YDR226W | *ADK1* | Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the mitochondria; | – | 2.11 |
| YHR068W | *DYS1* | Deoxyhypusine synthase, catalyzes formation of deoxyhypusine, the first step in hypusine biosynthesis; triggers posttranslational hypusination | – | 2.10 |
| YMR205C | *PFK2* | Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by | – | 2.09 |
| YDR432W | *NPL3* | RNA-binding protein that promotes elongation, regulates termination, and carries poly(A) mRNA from nucleus to cytoplasm; required for pre-mRNA | – | 2.08 |
| YNL233W | *BNI4* | Targeting subunit for Glc7p protein phosphatase, localized to the bud neck, required for localization of chitin synthase III to the bud neck via interaction with | – | 2.07 |
| YMR027W | *YMR027W* | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to | – | 2.06 |
| YDR111C | *ALT2* | Putative alanine transaminase (glutamic pyruvic | – | 2.06 |

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| YFL038C | *YPT1* | Rab family GTPase, involved in the ER-to-Golgi step of the secretory pathway; complex formation with the Rab escort protein Mrs6p is required for prenylation | – | 2.05 |
| YNR035C | *ARC35* | Subunit of the ARP2/3 complex, which is required for the motility and integrity of cortical actin patches; | – | 2.04 |
| YGL105W | *ARC1* | Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring | – | 2.04 |
| YNL010W | *YNL010W* | Putative protein of unknown function with similarity to phosphoserine phosphatases; green fluorescent protein (GFP)-fusion protein localizes to the | – | 2.04 |
| YPL032C | *SVL3* | Protein of unknown function, mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to | – | 2.02 |
| YDR510W | *SMT3* | Ubiquitin-like protein of the SUMO family, conjugated to lysine residues of target proteins; regulates chromatid cohesion, chromosome segregation, APC- | – | 2.01 |
| YDL185W | *TFP1* | Subunit A of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase; protein precursor undergoes self-catalyzed splicing to | – | 2.01 |
| YHL031C | *GOS1* | v-SNARE protein involved in Golgi transport, homolog | – | 2.01 |
| YML054C | *CYB2* | Cytochrome b2 (L-lactate cytochrome-c oxidoreductase), component of the mitochondrial intermembrane space, required for lactate utilization; | – | 2.00 |
| YGR279C | *SCW4* | Cell wall protein with similarity to glucanases; scw4 scw10 double mutants exhibit defects in mating | – | 2.00 |
| YOL164W | *BDS1* | Bacterially-derived sulfatase required for use of alkyl- | – | -2.00 |
| YGR074W | *SMD1* | Core Sm protein Sm D1; part of heteroheptameric complex (with Smb1p, Smd2p, Smd3p, Sme1p, Smx3p, and Smx2p) that is part of the spliceosomal | – | -2.00 |
| YMR126C | *DLT1* | Protein of unknown function, mutant sensitive to 6-azauracil (6AU) and mycophenolic acid (MPA) | – | -2.00 |
| YLR266C | *PDR8* | Transcription factor; targets include ATP-binding cassette (ABC) transporters, major facilitator superfamily transporters, and other genes involved in | – | -2.01 |
| YKR009C | *FOX2* | Multifunctional enzyme of the peroxisomal fatty acid beta-oxidation pathway; has 3-hydroxyacyl-CoA | – | -2.01 |
| YIL046W | *MET30* | F-box protein containing five copies of the WD40 motif, controls cell cycle function, sulfur metabolism, and methionine biosynthesis as part of the ubiquitin | – | -2.03 |
| YGR166W | *KRE11* | Subunit of TRAPPII, a multimeric guanine nucleotide-exchange factor for Ypt1p; involved in intra-Golgi traffic and the retrograde pathway from the | – | -2.04 |

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| YBR212W | *NGR1* | RNA binding protein that negatively regulates growth rate; interacts with the 3' UTR of the mitochondrial porin (POR1) mRNA and enhances its degradation; | – | -2.05 |
| YDL231C | *BRE4* | Zinc finger protein containing five transmembrane domains; null mutant exhibits strongly fragmented vacuoles and sensitivity to brefeldin A, a drug which is | – | -2.05 |
| YFR046C | *CNN1* | Kinetochore protein of unknown function; associated with the essential kinetochore proteins Nnf1p and | – | -2.06 |
| YMR132C | *JLP2* | Protein of unknown function, contains sequence that closely resembles a J domain (typified by the E. coli | – | -2.06 |
| YNL221C | *POP1* | Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors | – | -2.07 |
| YDL215C | *GDH2* | NAD(+)-dependent glutamate dehydrogenase, degrades glutamate to ammonia and alpha-ketoglutarate; expression sensitive to nitrogen | – | -2.08 |
| YER015W | *FAA2* | Medium chain fatty acyl-CoA synthetase, activates imported fatty acids; accepts a wide range of fatty acid chain lengths with a preference for medium | – | -2.09 |
| YOR004W | *UTP23* | Essential nucleolar protein that is a component of the SSU (small subunit) processome involved in 40S ribosomal subunit biogenesis; has homology to PINc | – | -2.09 |
| YFR025C | *HIS2* | Histidinolphosphatase, catalyzes the eighth step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts; | – | -2.10 |
| YLL048C | *YBT1* | Transporter of the ATP-binding cassette (ABC) family involved in bile acid transport; similar to mammalian | – | -2.10 |
| YER092W | *IES5* | Protein that associates with the INO80 chromatin remodeling complex under low-salt conditions | – | -2.11 |
| YNR074C | *AIF1* | Mitochondrial cell death effector that translocates to the nucleus in response to apoptotic stimuli, homolog | – | -2.11 |
| YJR050W | *ISY1* | Member of NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of spliceosome containing U2, U5, and U6 snRNAs, | – | -2.11 |
| YIR013C | *GAT4* | Protein containing GATA family zinc finger motifs | – | -2.12 |
| YLR193C | *UPS1* | Mitochondrial intermembrane space protein that regulates mitochondrial cardiolipin levels, null has defects in Mgm1p processing, integrity of | – | -2.12 |
| YGR280C | *PXR1* | Essential protein involved in rRNA and snoRNA maturation; competes with TLC1 RNA for binding to Est2p, suggesting a role in negative regulation of | – | -2.15 |
| YPR200C | *ARR2* | Arsenate reductase required for arsenate resistance; converts arsenate to arsenite which can then be | – | -2.16 |
| YDR249C | *YDR249C* | Putative protein of unknown function | – | -2.16 |

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| YOL044W | *PEX15* | Phosphorylated tail-anchored type II integral peroxisomal membrane protein required for peroxisome biogenesis, cells lacking Pex15p | – | -2.19 |
| YBL049W | *MOH1* | Protein of unknown function, has homology to kinase Snf7p; not required for growth on nonfermentable | – | -2.20 |
| YOR184W | *SER1* | 3-phosphoserine aminotransferase, catalyzes the formation of phosphoserine from 3-phosphohydroxypyruvate, required for serine and | – | -2.20 |
| YOL047C | *YOL047C* | Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the | – | -2.21 |
| YER040W | *GLN3* | Transcriptional activator of genes regulated by nitrogen catabolite repression (NCR), localization and | – | -2.21 |
| YPR168W | *NUT2* | Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; required for | – | -2.21 |
| YLR130C | *ZRT2* | Low-affinity zinc transporter of the plasma membrane; transcription is induced under low-zinc | – | -2.21 |
| YKL220C | *FRE2* | Ferric reductase and cupric reductase, reduces siderophore-bound iron and oxidized copper prior to uptake by transporters; expression induced by low | – | -2.22 |
| YLR004C | *THI73* | Putative plasma membrane permease proposed to be involved in carboxylic acid uptake and repressed by thiamine; substrate of Dbf2p/Mob1p kinase; | – | -2.22 |
| YOL084W | *PHM7* | Protein of unknown function, expression is regulated by phosphate levels; green fluorescent protein (GFP)- | – | -2.23 |
| YNL046W | *YNL046W* | Putative protein of unknown function; expression depends on Swi5p; GFP-fusion protein localizes to the endoplasmic reticulum; deletion confers sensitivity to | – | -2.25 |
| YDR257C | *RKM4* | Ribosomal lysine methyltransferase specific for monomethylation of Rpl42ap and Rpl42bp (lysine | – | -2.29 |
| YNL116W | *DMA2* | Protein involved in ubiquitination; plays a role in regulating spindle position and orientation; functionally redundant with Dma1p; orthologous to | – | -2.30 |
| YEL065W | *SIT1* | Ferrioxamine B transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; transcription is induced | – | -2.35 |
| YBR043C | *QDR3* | Multidrug transporter of the major facilitator superfamily, required for resistance to quinidine, | – | -2.37 |
| YNL129W | *NRK1* | Nicotinamide riboside kinase, catalyzes the phosphorylation of nicotinamide riboside and | – | -2.37 |
| YBL029W | *YBL029W* | Non-essential protein of unknown function | – | -2.38 |
| YPR128C | *ANT1* | Peroxisomal adenine nucleotide transporter; involved in beta-oxidation of medium-chain fatty acid; | – | -2.41 |

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| YBR166C | *TYR1* | Prephenate dehydrogenase involved in tyrosine biosynthesis, expression is dependent on | – | -2.41 |
| YLL027W | *ISA1* | Mitochondrial matrix protein involved in biogenesis of the iron-sulfur (Fe/S) cluster of Fe/S proteins, isa1 deletion causes loss of mitochondrial DNA and | – | -2.43 |
| YGL146C | *RRT6* | Putative protein of unknown function; non-essential gene identified in a screen for mutants with increased levels of rDNA transcription; contains two putative | – | -2.45 |
| YIL117C | *PRM5* | Pheromone-regulated protein, predicted to have 1 transmembrane segment; induced during cell | – | -2.46 |
| YBL103C | *RTG3* | Basic helix-loop-helix-leucine zipper (bHLH/Zip) transcription factor that forms a complex with | – | -2.46 |
| YDR090C | *YDR090C* | Putative protein of unknown function | – | -2.46 |
| YMR187C | *YMR187C* | Putative protein of unknown function; YMR187C is | – | -2.46 |
| YGR029W | *ERV1* | Flavin-linked sulfhydryl oxidase of the mitochondrial intermembrane space (IMS), oxidizes Mia40p as part of a disulfide relay system that promotes IMS | – | -2.47 |
| YDL121C | *YDL121C* | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to | – | -2.47 |
| YCR089W | *FIG2* | Cell wall adhesin, expressed specifically during mating; may be involved in maintenance of cell wall | – | -2.48 |
| YER039C | *HVG1* | Protein of unknown function, has homology to Vrg4p | – | -2.52 |
| YNL125C | *ESBP6* | Protein with similarity to monocarboxylate permeases, appears not to be involved in transport of | – | -2.53 |
| YAL044C | *GCV3* | H subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; also required for all protein | – | -2.53 |
| YBL095W | *YBL095W* | Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified | – | -2.54 |
| YHR160C | *PEX18* | Peroxin required for targeting of peroxisomal matrix proteins containing PTS2; interacts with Pex7p; | – | -2.54 |
| YBR115C | *LYS2* | Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to alpha-aminoadipate 6-semialdehyde, which is the fifth step | – | -2.55 |
| YGL205W | *POX1* | Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta-oxidation pathway; localized to the | – | -2.56 |
| YGL114W | *YGL114W* | Putative protein of unknown function; predicted member of the oligopeptide transporter (OPT) family | – | -2.62 |
| YFL021W | *GAT1* | Transcriptional activator of genes involved in nitrogen catabolite repression; contains a GATA-1-type zinc finger DNA-binding motif; activity and localization | – | -2.64 |
| YCR023C | *YCR023C* | Vacuolar membrane protein of unknown function; member of the multidrug resistance family; YCR023C | – | -2.64 |

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| YML097C | *VPS9* | A guanine nucleotide exchange factor involved in vesicle-mediated vacuolar protein transport; specifically stimulates the intrinsic guanine nucleotide | – | -2.66 |
| YOR221C | *MCT1* | Predicted malonyl-CoA:ACP transferase, putative component of a type-II mitochondrial fatty acid | – | -2.68 |
| YKL033W-A | *YKL033W-A* | Putative protein of unknown function; similar to | – | -2.75 |
| YLL057C | *JLP1* | Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase, involved in sulfonate catabolism for use as a sulfur source; contains sequence that resembles | – | -2.76 |
| YMR019W | *STB4* | Protein that binds Sin3p in a two-hybrid assay; contains a Zn(II)2Cys6 zinc finger domain characteristic of DNA-binding proteins; | – | -2.78 |
| YBR248C | *HIS7* | Imidazole glycerol phosphate synthase (glutamine amidotransferase:cyclase), catalyzes the fifth and sixth steps of histidine biosynthesis and also produces | – | -2.82 |
| YNR065C | *YNR065C* | Protein of unknown function; protein-protein interactions suggest a possible role in actin patch | – | -2.84 |
| YOR339C | *UBC11* | Ubiquitin-conjugating enzyme most similar in sequence to Xenopus ubiquitin-conjugating enzyme E2-C, but not a true functional homolog of this E2; | – | -2.86 |
| YOR008C-A | *YOR008C-A* | Putative protein of unknown function, includes a potential transmembrane domain; deletion results in | – | -2.87 |
| YDR384C | *ATO3* | Plasma membrane protein, regulation pattern suggests a possible role in export of ammonia from the cell; phosphorylated in mitochondria; member of | – | -2.89 |
| YBR249C | *ARO4* | 3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase, catalyzes the first step in aromatic amino acid biosynthesis and is feedback-inhibited by | – | -2.91 |
| YGR121C | *MEP1* | Ammonium permease; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport only ammonium (NH4+); expression is under the | – | -2.92 |
| YPL052W | *OAZ1* | Regulator of ornithine decarboxylase (Spe1p), antizyme that binds to Spe1p to regulate ubiquitin-independent degradation; ribosomal frameshifting | – | -2.95 |
| YBL071W-A | *KTI11* | Zn-ribbon protein that co-purifies with Dph1 and Dph2 in a complex required for synthesis of diphthamide on translation factor eEF2 and with | – | -2.96 |
| YER055C | *HIS1* | ATP phosphoribosyltransferase, a hexameric enzyme, catalyzes the first step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity | – | -2.97 |
| YIR034C | *LYS1* | Saccharopine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of saccharopine to L-lysine, which is the final step in the lysine | – | -2.98 |

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| YER184C | *YER184C* | Putative zinc cluster protein; deletion confers sensitivity to Calcufluor white, and prevents growth | – | -3.03 |
| YDR487C | *RIB3* | 3,4-dihydroxy-2-butanone-4-phosphate synthase (DHBP synthase), required for riboflavin biosynthesis from ribulose-5-phosphate, also has an unrelated | – | -3.03 |
| YDR076W | *RAD55* | Protein that stimulates strand exchange by stabilizing the binding of Rad51p to single-stranded DNA; involved in the recombinational repair of double- | – | -3.05 |
| YNL311C | *YNL311C* | F-box protein of unknown function predicted to be part of an SCF ubiquitin protease complex; involved in regulating protein levels of sulfur metabolism | – | -3.11 |
| YPL135W | *ISU1* | Conserved protein of the mitochondrial matrix, performs a scaffolding function during assembly of iron-sulfur clusters, interacts physically and | – | -3.13 |
| YGR197C | *SNG1* | Protein involved in resistance to nitrosoguanidine (MNNG) and 6-azauracil (6-AU); expression is | – | -3.13 |
| YLR090W | *XDJ1* | Putative chaperone, homolog of E. coli DnaJ, closely related to Ydj1p; the authentic, non-tagged protein is | – | -3.14 |
| YGL154C | *LYS5* | Phosphopantetheinyl transferase involved in lysine biosynthesis; converts inactive apo-form of Lys2p (alpha-aminoadipate reductase) into catalytically | – | -3.23 |
| YLR348C | *DIC1* | Mitochondrial dicarboxylate carrier, integral membrane protein, catalyzes a dicarboxylate-phosphate exchange across the inner mitochondrial | – | -3.25 |
| YOR192C | *THI72* | Transporter of thiamine or related compound; shares | – | -3.27 |
| YJR010W | *MET3* | ATP sulfurylase, catalyzes the primary step of intracellular sulfate activation, essential for | – | -3.33 |
| YGR154C | *GTO1* | Omega-class glutathione transferase; induced under oxidative stress; putative peroxisomal localization | – | -3.34 |
| YHR208W | *BAT1* | Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly | – | -3.37 |
| YER039C-A | *YER039C-A* | Putative protein of unknown function; YER039C-A is | – | -3.37 |
| YGL186C | *TPN1* | Plasma membrane pyridoxine (vitamin B6) transporter; member of the purine-cytosine permease subfamily within the major facilitator | – | -3.38 |
| YHR122W | *YHR122W* | Protein of unknown function required for establishment of sister chromatid cohesion; synthetically lethal with RFC5, an RF-C subunit that | – | -3.41 |
| YKL211C | *TRP3* | Bifunctional enzyme exhibiting both indole-3-glycerol-phosphate synthase and anthranilate synthase activities, forms multifunctional hetero-oligomeric | – | -3.43 |
| YPR078C | *YPR078C* | Putative protein of unknown function; possible role in DNA metabolism and/or in genome stability; | – | -3.45 |

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| YDL054C | *MCH1* | Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma | – | -3.51 |
| YLR042C | *YLR042C* | Protein of unknown function; localizes to the | – | -3.58 |
| YOR161C | *PNS1* | Protein of unknown function; has similarity to Torpedo californica tCTL1p, which is postulated to be | – | -3.59 |
| YJR155W | *AAD10* | Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase; | – | -3.59 |
| YPL188W | *POS5* | Mitochondrial NADH kinase, phosphorylates NADH; also phosphorylates NAD(+) with lower specificity; | – | -3.60 |
| YGL059W | *PKP2* | Mitochondrial protein kinase that negatively regulates activity of the pyruvate dehydrogenase complex by phosphorylating the ser-133 residue of | – | -3.63 |
| YBR105C | *VID24* | Peripheral membrane protein located at Vid (vacuole import and degradation) vesicles; regulates fructose-1,6-bisphosphatase (FBPase) targeting to the vacuole; | – | -3.67 |
| YKR071C | *DRE2* | Conserved component of an early step in the cytosolic Fe-S protein assembly (CIA) machinery; contains an Fe-S cluster that receives electrons from | – | -3.70 |
| YBR104W | *YMC2* | Mitochondrial protein, putative inner membrane transporter with a role in oleate metabolism and glutamate biosynthesis; member of the | – | -3.74 |
| YJL072C | *PSF2* | Subunit of the GINS complex (Sld5p, Psf1p, Psf2p, Psf3p), which is localized to DNA replication origins | – | -3.81 |
| YDR158W | *HOM2* | Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression | – | -3.82 |
| YPL273W | *SAM4* | S-adenosylmethionine-homocysteine methyltransferase, functions along with Mht1p in the conversion of S-adenosylmethionine (AdoMet) to | – | -3.83 |
| YPL033C | *SRL4* | Protein of unknown function; involved in regulation of dNTP production; null mutant suppresses the | – | -3.84 |
| YCL030C | *HIS4* | Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase | – | -3.85 |
| YNL036W | *NCE103* | Carbonic anhydrase; poorly transcribed under aerobic conditions and at an undetectable level under | – | -3.86 |
| YBR045C | *GIP1* | Meiosis-specific regulatory subunit of the Glc7p protein phosphatase, regulates spore wall formation and septin organization, required for expression of | – | -3.88 |
| YER056C | *FCY2* | Purine-cytosine permease, mediates purine (adenine, guanine, and hypoxanthine) and cytosine | – | -4.04 |
| YMR321C | *YMR321C* | Putative protein of unknown function; proposed to | – | -4.07 |

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| YHR018C | *ARG4* | Argininosuccinate lyase, catalyzes the final step in the | – | -4.10 |
| YPR058W | *YMC1* | Mitochondrial protein, putative inner membrane transporter with a role in oleate metabolism and glutamate biosynthesis; member of the | – | -4.10 |
| YOL141W | *PPM2* | AdoMet-dependent tRNA methyltransferase also involved in methoxycarbonylation; required for the synthesis of wybutosine (yW), a modified guanosine | – | -4.15 |
| YKL218C | *SRY1* | 3-hydroxyaspartate dehydratase, deaminates L-threo-3-hydroxyaspartate to form oxaloacetate and ammonia; required in the presence of | – | -4.31 |
| YOL091W | *SPO21* | Component of the meiotic outer plaque of the spindle pole body, involved in modifying the meiotic | – | -4.32 |
| YDR253C | *MET32* | Zinc-finger DNA-binding protein, involved in transcriptional regulation of the methionine | – | -4.35 |
| YPL252C | *YAH1* | Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur proteins; involved in | – | -4.39 |
| YIL056W | *VHR1* | Transcriptional activator, required for the vitamin H-responsive element (VHRE) mediated induction of VHT1 (Vitamin H transporter) and BIO5 (biotin | – | -4.41 |
| YOR303W | *CPA1* | Small subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor; translationally regulated by an | – | -4.45 |
| YDR354W | *TRP4* | Anthranilate phosphoribosyl transferase of the tryptophan biosynthetic pathway, catalyzes the phosphoribosylation of anthranilate, subject to the | – | -4.58 |
| YOR130C | *ORT1* | Ornithine transporter of the mitochondrial inner membrane, exports ornithine from mitochondria as part of arginine biosynthesis; human ortholog is | – | -4.59 |
| YER060W-A | *FCY22* | Putative purine-cytosine permease, very similar to | – | -4.59 |
| YNR057C | *BIO4* | Dethiobiotin synthetase, catalyzes the third step in the biotin biosynthesis pathway; BIO4 is in a cluster of 3 genes (BIO3, BIO4, and BIO5) that mediate biotin | – | -4.68 |
| YGL224C | *SDT1* | Pyrimidine nucleotidase; overexpression suppresses the 6-AU sensitivity of transcription elongation factor | – | -4.89 |
| YNL095C | *YNL095C* | Putative protein of unknown function predicted to contain a transmembrane domain; YNL095C is not an | – | -4.94 |
| YMR062C | *ARG7* | Mitochondrial ornithine acetyltransferase, catalyzes the fifth step in arginine biosynthesis; also possesses acetylglutamate synthase activity, regenerates | – | -4.99 |
| YJL198W | *PHO90* | Low-affinity phosphate transporter; deletion of pho84, pho87, pho89, pho90, and pho91 causes synthetic lethality; transcription independent of Pi | – | -5.08 |
| YOR302W | *YOR302W* | CPA1 uORF, Arginine attenuator peptide, regulates | – | -5.18 |

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| YOL058W | *ARG1* | Arginosuccinate synthetase, catalyzes the formation of L-argininosuccinate from citrulline and L-aspartate | – | -5.19 |
| YBR256C | *RIB5* | Riboflavin synthase; catalyzes the last step of the | – | -5.28 |
| YDL198C | *GGC1* | Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in | – | -5.29 |
| YOR032C | *HMS1* | Basic helix-loop-helix (bHLH) protein with similarity to myc-family transcription factors; overexpression confers hyperfilamentous growth and suppresses the | – | -5.29 |
| YIR017C | *MET28* | Basic leucine zipper (bZIP) transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in | – | -5.33 |
| YLR089C | *ALT1* | Alanine transaminase (glutamic pyruvic transaminase); involved in alanine biosynthetic and catabolic processes; the authentic, non-tagged | – | -5.33 |
| YJR111C | *YJR111C* | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to | – | -5.38 |
| YJR154W | *YJR154W* | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to | – | -5.49 |
| YJR137C | *MET5* | Sulfite reductase beta subunit, involved in amino acid biosynthesis, transcription repressed by methionine | – | -5.66 |
| YNL104C | *LEU4* | Alpha-isopropylmalate synthase (2-isopropylmalate synthase); the main isozyme responsible for the first | – | -5.87 |
| YER174C | *GRX4* | Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase; monothiol glutaredoxin subfamily member along with Grx3p and | – | -5.88 |
| YPR167C | *MET16* | 3'-phosphoadenylsulfate reductase, reduces 3'-phosphoadenylyl sulfate to adenosine-3',5'-bisphosphate and free sulfite using reduced | – | -5.95 |
| YJR109C | *CPA2* | Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an | – | -6.23 |
| YER024W | *YAT2* | Carnitine acetyltransferase; has similarity to Yat1p, which is a carnitine acetyltransferase associated with | – | -6.25 |
| YNR068C | *YNR068C* | Putative protein of unknown function | – | -6.35 |
| YKR069W | *MET1* | S-adenosyl-L-methionine uroporphyrinogen III transmethylase, involved in the biosynthesis of siroheme, a prosthetic group used by sulfite | – | -6.40 |
| YER069W | *ARG5,6* | Protein that is processed in the mitochondrion to yield acetylglutamate kinase and N-acetyl-gamma-glutamyl-phosphate reductase, which catalyze the | – | -6.44 |
| YKL029C | *MAE1* | Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for | – | -6.47 |
| YML116W | *ATR1* | Multidrug efflux pump of the major facilitator superfamily, required for resistance to aminotriazole | – | -6.51 |

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| YGR065C | *VHT1* | High-affinity plasma membrane H+-biotin (vitamin H) symporter; mutation results in fatty acid auxotrophy; 12 transmembrane domain containing major | – | -6.60 |
| YJR130C | *STR2* | Cystathionine gamma-synthase, converts cysteine | – | -6.63 |
| YLR092W | *SUL2* | High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of | – | -6.83 |
| YMR108W | *ILV2* | Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the | – | -6.90 |
| YOL140W | *ARG8* | Acetylornithine aminotransferase, catalyzes the fourth step in the biosynthesis of the arginine | – | -7.11 |
| YPL264C | *YPL264C* | Putative membrane protein of unknown function; physically interacts with Hsp82p; YPL264C is not an | – | -7.16 |
| YOL119C | *MCH4* | Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma | – | -7.39 |
| YPR027C | *YPR027C* | Putative protein of unknown function | – | -7.46 |
| YGR224W | *AZR1* | Plasma membrane transporter of the major facilitator superfamily, involved in resistance to azole drugs | – | -7.62 |
| YFR030W | *MET10* | Subunit alpha of assimilatory sulfite reductase, which | – | -7.71 |
| YHR071W | *PCL5* | Cyclin, interacts with and phosphorylated by Pho85p cyclin-dependent kinase (Cdk), induced by Gcn4p at level of transcription, specifically required for Gcn4p | – | -7.71 |
| YNR058W | *BIO3* | 7,8-diamino-pelargonic acid aminotransferase (DAPA), catalyzes the second step in the biotin biosynthesis pathway; BIO3 is in a cluster of 3 genes | – | -8.23 |
| YBR296C | *PHO89* | Na+/Pi cotransporter, active in early growth phase; similar to phosphate transporters of Neurospora | – | -9.20 |
| YHR029C | *YHI9* | Protein of unknown function; null mutant is defective in unfolded protein response; possibly involved in a membrane regulation metabolic pathway; member of | – | -9.30 |
| YER175C | *TMT1* | Trans-aconitate methyltransferase, cytosolic enzyme that catalyzes the methyl esterification of 3-isopropylmalate, an intermediate of the leucine | – | -9.72 |
| YGL117W | *YGL117W* | Putative protein of unknown function | – | -9.72 |
| YGL184C | *STR3* | Cystathionine beta-lyase, converts cystathionine into | – | -9.83 |
| YBR148W | *YSW1* | Protein required for normal prospore membrane formation; interacts with Gip1p, which is the meiosis-specific regulatory subunit of the Glc7p protein | – | -10.31 |
| YBR047W | *FMP23* | Putative protein of unknown function; proposed to be involved in iron or copper homeostasis; the authentic, non-tagged protein is detected in highly | – | -12.46 |

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| YJL088W | *ARG3* | Ornithine carbamoyltransferase (carbamoylphosphate:L-ornithine | – | -14.12 |
| YMR096W | *SNZ1* | Protein involved in vitamin B6 biosynthesis; member of a stationary phase-induced gene family; coregulated with SNO1; interacts with Sno1p and | – | -17.82 |
| YPL250C | *ICY2* | Protein of unknown function; mobilized into polysomes upon a shift from a fermentable to | – | -18.06 |
| YDR380W | *ARO10* | Phenylpyruvate decarboxylase, catalyzes decarboxylation of phenylpyruvate to | – | -25.87 |
| YMR095C | *SNO1* | Protein of unconfirmed function, involved in pyridoxine metabolism; expression is induced during stationary phase; forms a putative glutamine | – | -33.55 |
| YBR294W | *SUL1* | High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of | – | -39.15 |